AUTHOR INDEX

to Volume 145, January–April 1997

Allendorf, F. W., 1083
Ambrosio, L., 163
Ankenbauer, R. G., 543
Ansorge, W., 627
Aquadro, C. F., 1053
Arcá, B., 267
Ardlie, K., 1093
Arkhipova, I., 729

Bachellier, S., 551
Bachhawat, A. K., 75
Baek, K.-H., 163
Baker, S. C., 1109
Baker, S. H., 615
Balding, D. J., 505
Barkan, A., 467
Barreau, G., 1171
Barton, N. H., 493
Begun, D. J., 375
Bender, W., 123
Benes, V., 627
Benson, N. R., 17
Bergelson, J., 807
Bergman, A., 207
Bijma, P., 1243
Bland, A. E., 435
Bloecher, A., 615
Boeke, J. D., 911
Boguta, M., 595
Bonnefoy, N., 903
Bonner, M. R., 787
Bovenhuis, H., 1243
Boyce, W. M., 421
Boynton, J. E., 97
Brascamp, E. W., 395
Brenner, C. H., 535
Brill, S. J., 891
Britton, R. A., 867
Broach, J. R., 605
Brown, W. M., 383
Buckler, E. S., IV, 821
Buss, L. W., 861
Buttel, L., 1093

Cameron, V. L., 903
Casares, F., 123
Cerutti, H., 97
Charlesworth, B., 989, 1015
Charlesworth, D., 989
Chaudhuri, B., 75
Chen, X., 935
Cherbas, L., 349
Cherbas, P., 349
Cherest, H., 627
Chiu, Y.-H., 707
Chory, J., 1125
Ciccarese, S., 409
Clément, J.-M., 551
Cook, K. R., 737
Cooley, L., 1063
Corces, V. G., 153
Cortopassi, G. A., 771
Coyne, J. A., 1015, 1031
Craig, N. L., 573

Dabert, P., 877
Danzmann, R. G., 1083
Davidian, J.-C., 627
Dean, N., 637
de Cuevas, M., 297
de Visser, J. A. G. M. (Arjan), 815
Donaldson, K. M., 325
Donnelly, P., 505
Donovan, J. D., 85
Ducousso, A., 1229
Durand, D., 1093
Dübendorfer, A., 173

Ehrenhofer-Murray, A. E., 923
Engels, W. R., 11
Enomoto, M., 563
Epps, J. L., 1041
Evans, D. R. H., 227

Fan, Q.-Q., 661
Feldman, M. W., 207
Ferguson, D. O., 243
Findley, S. D., 297
Fink, G. R., 671
Fleming, R. J., 359
Fox, T. D., 903
Frederick, D. L., 615
Friis, T., 685

Gach, M. H., 383
Gaiser, J. C., 1109
Galibert, F., 637
Garvik, B. M., 45
Gasser, C. S., 1109
Gdula, D. A., 153
Gelbart, W. M., 297
Gillham, N. W., 97
Gilson, E., 551
Goldstein, D. B., 207
Goodwin, R., 1031
Gorbunova, V., 1161
Gómez-Chiarri, M., 759
Griffiths, R. C., 505
Grigliatti, T. A., 945
Grosberg, R. K., 857
Guo, S.-W., 1201
Guttman, D. S., 989

Hall, B. G., 39
Hall, J. C., 1003
Hamblin, M. T., 1053
Hammer, M. F., 787
Hart, M. W., 857
Hartwell, L. H., 45
Hawley, R. S., 1031
Heath, S. C., 1171
Hediger, M., 173
Hedrick, P. W., 421
Hermankova, M., 911
Hey, J., 833, 847
Hnilicka, J., 989
Hoekstra, R. F., 815
Hofnung, M., 551
Holmes, S. G., 605
Holtsford, T. P., 821
Hopper, A. K., 595
Horai, S., 787
Hudson, A. M., 1063
Hughes, K. A., 139
Hukriede, N. A., 359
Hutchin, T. P., 771

Ingavale, S., 75
Ippolito, A., 821
Issel-Tarver, L., 185

Janss, L. L. G., 395
Jenkins, T., 787
Johnson, A. L., 85
Johnson, A. M., 97
Johnson, G., 777

Johnston, L. H., 85
Jones, J. B., 1041

Kadyk, L. C., 111
Kaifu, M., 749
Kalinowski, S., 421
Karafet, T., 787
Karpen, G. H., 325, 737
Kimble, J., 111
Kindle, K. L., 935
Kinghorn, B. P., 479
Kingsley, D. M., 435
Kmiec, E. B., 243
Kobayashi, T., 749
Koll, F., 697
Kotani, H., 243
Kremer, A., 1229
Krone, S. M., 519

Lambie, E. J., 111
Lanave, C., 409
Last, R. L., 197
Lauermann, V., 911
Laurie, C. C., 339
Levin, S. A., 1093
Levitan, D. R., 857
Levy, A. A., 1161
Lewontin, R. C., 311
Li, J., 197, 729
Li, W., 63
Li, Z., 453, 1139
Liu, J., 339
Lloyd, V. K., 945
Lobo, Z., 587
Long, M., 311
Loukeris, T. G., 267
Lukaszewski, A. J., 1155
Lupski, J. R., 867

Madden, L. D., 1031
Maitra, P. K., 587
Malaspina, P., 787
Maniar, H. S., 891
Manus, V., 637
Margulies, R. U., 45
Marker, P. C., 435
Martin, N. C., 595
Meirelles, F. V., 445
Mendel, J. E., 715
Mendel-Hartvig, J., 467
Mercer, J. M., 339
Merriam, J., 123
Meselson, M., 729
Meyerowitz, E. M., 5
Mhaiskar, V., 637
Mi Lee, Y., 605
Mitchell, A. P., 63
Mitchell, R. J., 787
Mokady, O., 861
Morris, N. R., 707
Mösch, H.-U., 671
Muggli-Cockett, N. E., 421
Mukaihara, T., 563
Murphy, T. D., 737

Nagylaki, T., 485
Neiman, A. M., 637
Neuhauser, C., 519
Newfeld, S. J., 297
Nguyen, T. C., 737
Nishikawa, K., 749
Nitasaka, E., 311
Norris, D., 647
Novelletto, A., 787
Novotny, C. P., 253
Nöthiger, R., 173
Numachi, K.-I., 749

Orr, H. A., 1031
Osier, M., 253
Overholtzer, M. H., 903

Padgett, R. W., 297
Park, W. D., 453, 1139
Paterson, A. H., 453, 1139
Pauli, D., 975
Paulovich, A. G., 45
Peck, J. R., 1171
Peixoto, A. A., 1003
Penedo, M. C. T., 421
Pennetta, G., 975
Pepper, A. E., 1125
Petes, T. D., 661
Piálek, J., 493
Pinson, S. R. M., 453, 1139
Plasterk, R. H. A., 715
Pollock, D. D., 207
Porter, G., 29
Powers, D. A., 759
Preer, J. R., Jr., 217
Purrington, C. B., 807

Radke, K., 163
Radman, M., 29
Ramey, R. R., II, 421
Ranz, J. M., 281
Rendi, M. H., 243
Resnick, M. A., 29
Reyero, M.-I., 1073
Rice, M. C., 243
Richter, B., 311
Richter, B. G., 297
Rine, J., 185, 923
Rivier, D. H., 923
Robinson, D. N., 1063
Robinson-Beers, K., 1109
Rose, A. B., 197, 605
Ross, K. G., 961
Rossignol, M., 697
Roth, J., 17
Rousset, F., 1219
Ruiz, A., 281
Russell, L. B., 435

Saavedra, C., 1073
Saccone, C., 409
Saez, E., 605
Sanicola, M., 297
Savakis, C., 267
Sayegh, S., 605
Sánchez-Herrero, E., 123
Schmidt, R., 173
Schulte, P. M., 759
Segarra, C., 281
Segawa, R., 749
Seung, K., 435
Silar, P., 697
Silver, L. M., 1093
Simon, L., 647
Simpson, C. L., 935
Sinclair, D. A., 945
Smith, G. R., 877
Smith, L. A., 1003
Smith, L. C., 445
Smith-Leiker, T. A., 1063
Sokol, N. S., 1063
Spurdle, A. B., 787
Stadler, D., 863
Stansel, J. W., 453, 1139
Stark, M. J. R., 227
Steinemann, M., 261
Steinemann, S., 261
Stellwagen, A. E., 573
Stern, D. B., 935
Sternberg, P. W., 715
Steuerle, K., 605
Surdin-Kerjan, Y., 627

Tanda, S., 1041
Tatchell, K., 615
Tavaré, S., 505
Terrett, J. A., 749
Thomas, D., 627
Thomas, R. H., 749
Thon, G., 685
Tobiasz, A., 595
Toone, W. M., 85

Torello, A. T., 903
Toyn, J. H., 85
Troyer, A. F., 1149
True, J. R., 339
Tsui, K., 647

Ueda, T., 749
Ueshima, R., 749
Ullrich, R. C., 253

Vaduva, G., 595
Van Arendonk, J. A. M., 395, 1243
van den Ende, H., 815
Velmurugan, S., 587
Villanueva, J. M., 1109
Voelker, R., 467

Wakeley, J., 833, 847
Watanabe, K., 749
Westmoreland, J., 29
White, M. A., 661
Wilson, R., 891
Wood, E. T., 787
Wu, T. T., 777

Xiong, M., 1201
Xu, F., 661

Yamazaki, N., 749
Yokobori, S.-I., 749
Yu, A., 989
Yue, CH., 253

Zabalou, S., 267
Zanetto, A., 1229
Zegura, S. L., 787
Zouros, E., 1073
Zwaal, R. R., 715
Żoładek, T., 595

SUBJECT INDEX

to Volume 145, January-April 1997

Actin cytoskeleton, *Saccharomyces cerevisiae* PPH2 mutants, 227
Adaptive mutations, specificity, 39
Advantageous alleles, spread across barriers, 493
Albinaria coerulea, gene organization, 749
Alcohol dehydrogenase, *Adh* gene origin and evolution in *Drosophila*, 375
Allogenicity, specificity in *Hydractinia symbiolongicarpus*, control of (*letter*), 857
Animal models, mitochondrial genotype segregation in heteroplasmic lineage, embryonic karyoplast transplantation producing, 445
Antibiotic resistance, in *Arabidopsis thaliana*, fitness consequences, 807
Arabidopsis thaliana
  det1 mutant, identification of elements of flowering-time and light-response regulatory pathways by extragenic suppressors of, 1125
  herbicide and antibiotic resistance in, fitness consequences, 807
  ovule development in, interaction among genes regulating, 1109
  trp1 mutants, 197
Artiodactyls, constant T-cell receptor evolution, 409
Aspergillus nidulans, nuclear migration in, $tRNA^{Leu}$ missense suppressor of nudC3 blocking, 707

Bacterial interspersed mosaic elements (BIMEs), sequence polymorphism in *Escherichia coli*, 551
Bighorn sheep, major histocompatibility complex and microsatellite loci variation, 421
Breeding value, estimation from data containing inbred individuals in common carp, 1243

Caenorhabditis elegans
  chemosensation of dauer-inducing pheromone, G proteins involved in, 715
  mitotic and meiotic requirement for *glp-3*, 111
Calcium channel genes, of *Drosophila melanogaster*, genomic organization and evolution of alternative exons in, 1003
Carp, breeding value and variance component estimation from data containing inbred individuals, 1243
Cell cycle, exit from mitosis, *Saccharomyces cerevisiae* Swi5 regulation, 85
Cell integrity, *Saccharomyces cerevisiae* PPH2 mutants, 227
Centromeres, *Drosophila melanogaster*, identification of *trans*-acting genes necessary for function, 737
Cepaea nemoralis, gene organization, 749
Chemosensation, of *Caenorhabditis elegans* dauer-inducing pheromone, G proteins involved in, 715
Chlamydomonas moewussii, test for synergistic epistasis in, 815
Chlamydomonas reinhardtii
  nuclear expression of foreign genes in, 95
  translational defects, *SIM30* mutation suppression of, 935
Chromosomal evolution, mapping of Muller's elements D and E in *Drosophila repleta*, 281
Chromosomes
  asymmetrical isochromosome development and meiotic behavior in wheat, 1155
  loss caused by *SIR* gene hyperactivation, 605
  Y. *See* Y chromosomes
Coalescence times, inference from DNA sequence data, 505
Computer programs, Kinship Program, 535
Conjugation (*Perspectives*), 543
Corn. *See* Maize
Culaea inconstans, mitochondrial DNA duplications, 383
Cyprinus carpio, breeding value and variance component estimation from data containing inbred individuals, 1243
Cytochrome *c* oxidase subunit II, *Saccharomyces cerevisiae*, deletion of leader peptide of precursor of, 903

Deafness, mitochondrial mutation conferring, origins, 771
Deletion, between *Salmonella typhimurium* flagellin genes, 551
Development, logic in plants, 5
Developmental genetics, *Drosophila* hybrid inviability, 1031
Distance models, genetic differentiation and estimation of gene flow from *F*-statistics under isolation, 1219
DNA
  inference of coalescence times from intraspecies sequences, 505
  mitochondrial
    duplications in *Culaea inconstans*, 383
    segregation in mice, embryonic karyoplast transplantation producing, 445
  ribosomal, evolution of, divergent paralogues and phylogenetic implications, 821
DNA damage, in *Saccharomyces cerevisiae*, requirements for S phase regulation in response to, 45
DNA repair, *Ustilago maydis REC2* and *RAD51* genes, 243
DNA replication forks, movement in *Saccharomyces cerevisiae*, replication Protein-A subunits in, 891
Drosophila americana americana, neo-Y-chromosome, lack of degeneration of loci on, 989
Drosophila mauritiana
  morphological difference between *Drosophila simulans* and, introgression analysis of quantitative trait loci contributing to, 339

sexual difference between *Drosophila sechellia* and, pheromonal
difference affecting, 1015
Drosophila melanogaster
calcium channel genes of, genomic organization and evolution of alternative exons in, 1003
centromere function, identification of *trans*-acting genes necessary for, 737
decapentaplegic gene
molecular evolution, 297
sequence of polymorphism and species divergence, 311
female, survival, sex determination, and differentiation in, 975
glucose dehydrogenase locus nucleotide sequence variation in, 1053
heterochromatic factors in, competition among variegating rearrangements for, 945
Minos transposon mobilization, 267
oroshigane functions in hedgehog signal transduction, 1041
P element invasions (*Perspectives*), 1111
Ser antimorph characterization, 359
sperm precedence quantitative genetics, 139
stand still gene, 975
Drosophila miranda, TRAM retransposon location, 261
Drosophila repleta, Muller's elements D and E, mapping, 281
Drosophila sechellia, sexual difference between *Drosophila mauritiana* and, pheromonal difference affecting, 1015
Drosophila simulans, morphological difference between *Drosophila mauritiana* and, introgression analysis of quantitative trait loci contributing to, 339
Drosophila spp.
D-raf effects on torso signal transduction, 163
gene-dosage compensation mode, 729
hybrid inviability, 1031
ovarian ring canal inner rim formation dependence on *cheerio,* 1063
"parahomologous" gene targeting, 349
repleta group, *Adh* gene origin and evolution, 375
silencing effect of *mod(mdg4)* mutations in, characterization of functional domains of su(Hw) protein mediating, 153
trans-suppression of terminal deficiency-associated position effect variegation in minimicrosomes, 325
Ultrabithorax interaction with native and foreign promoters, 123

Epigenetics, inheritance of transcriptional silencing and switching competence in fission yeast, 685
Epistasis
quantitative trait loci in rice, 453
synergistic, experimental test for, in *Chlamydomonas moewussii,* 815

Escherichia coli
dnaG mutations in, isolation and characterization of suppressors, 867
mismatch repair in, transformation by highly mismatched molecules resembling recombination intermediates, 29
sequence polymorphism in, bacterial interspersed mosaic elements as source, 551
specificity of adaptive mutations, 39
wild-type, enhancement of gene replacement with linear fragments by Chi sites, 877
Euhadra herklotsi, gene organization, 749
Exons, *Drosophila melanogaster* calcium channel genes, evolution of, 1003

Fire ants, multilocus evolution in, 961
Fundulus heteroclitus, Ldh-B structure and function in promoter and 5′ flanking regions, 759

Gastropods, pulmonate, gene organization, 749
Gene(s)
Adh, origin and evolution, 375
ANT, interaction with other genes regulating ovule development in *Arabidopsis thaliana,* 1109
apd1^{+}, glutathione biosynthesis in yeasts, 75
Bmp5, mutations in mice, 435
calcium channel, of *Drosophila melanogaster,* genomic organization and evolution of alternative exons in, 1003
cheerio, Drosophila ovarian ring canal inner rim formation dependence on, 1063
decapentaplegic (*dpp*)
molecular evolution in *Drosophila melanogaster,* 297
sequence of polymorphism and species divergence in *Drosophila melanogaster,* 311
D-raf, torso signal transduction in *Drosophila,* 163
foreign, nuclear expression in *Chlamydomonas reinhardtii,* 95
glp-3, Caenorhabditis elegans requirement for mitosis and meiosis, 111
governing long first internode of corn, location of, 1149
histone H2A-H2B dimer concentration and progression into meiosis in *Saccharomyces cerevisiae,* 647
immunoglobulin V-genes, method of estimating numbers in mice and humans, 777
INO, interaction with other genes regulating ovule development in *Arabidopsis thaliana,* 1109
Ldh-B, structure and function in promoter and 5′ flanking regions of *Fundulus heteroclitus,* 759
MDH-B, secondary tetrasomic segregation *MDH-B* and preferential pairing of homeologues in rainbow trout, 1083
MDP1, identity with *RSP4,* 595
mutations. *See* Mutants/mutations nature of, ultraviolet-induced mutations and, 863
olfactory, mammalian evolution, 185

oroshigane, functions in hedgehog signal transduction, 1041
pdc2, pyruvate decarboxylase synthesis in *Saccharomyces cerevisiae*, 587
PKC1, glycosyltransferase encoding in *Saccharomyces cerevisiae*, 637
RAD51, DNA repair and mitotic recombination in *Ustilago maydis*, 243
RAD9, RAD *17*, and *RAD24*, S phase regulation in response to DNA damage in *Saccharomyces cerevisiae*, 45
REC2, DNA repair and mitotic recombination in *Ustilago maydis*, 243
Rim1p, sporulation regulation in yeasts, 63
RSP4, identity with *MDP1*, 595
Sas2, role in silencing and origin recognition complex functioning, 923
Ser, Beaded of Goldschmidt antimorphic allele, encoding of protein lacking transmembrane and intracellular domains, 359
sex-determining, *masculinizer* mutation definition in *Musca domestica*, 173
Sic1, *Saccharomyces cerevisiae* Swi5 regulation, 85
single, affecting meat quality traits in pigs, Bayesian statistical analysis for, 395
SIR, chromosome loss caused by hyperactivation of, 605
stand still, 975
su(Hw), characterization of functional domains mediating silencing effect of *mod(mdg4)* mutations in *Drosophila*, 153
tha1, in vivo role of cp-SecA in thylakoid protein targeting, 467
trans-acting, necessary for centromere function in *Drosophila melanogaster*, identification, 737
Ultrabithorax (*Ubx*), regulatory region interaction with native and foreign promoters, 123
Gene-dosage compensation, *Drosophila*, 729
Gene expression, *decapentaplegic* gene, in *Drosophila melanogaster* development, 297
Gene flow
estimation from *F*-statistics under isolation by distance, 1219
multilocus evolution in fire ants, 961
Gene markers, multilocus and multitrait measures of differentiation for, 1229
Gene organization, pulmonate gastropods, 749
Gene replacement, in wild-type *Escherichia coli*, enhancement by Chi sites, 877
Gene targeting, "parahomologous," in *Drosophila*, 349
Genetic degeneration, in neo-Y-chromosome of *Drosophila americana americana*, lack of, 989
Genetic differentiation
under isolation by distance, 1219
multilocus and multitrait measures, 1229
Genetics Society of America, Thomas Hunt Morgan Medal awarded to Franklin W. Stahl, 1
Genetics Society of America Medal
awarded to Elliot Meyerowitz, 1
essay, plants and the logic of development, 5
Genomic organization, of *Drosophila melanogaster* calcium channel genes, 1003
Genotype probability index, derived from segregation analysis, 479
Glutathione, biosynthesis in yeasts, *apd1*$^{+}$ encoding of enzyme required for, 75
Glycosyltransferases, *PKC1* encoding in *Saccharomyces cerevisiae*, 637
G proteins, chemosensation of *Caenorhabditis elegans* dauer-inducing pheromone, 715
Growth, filamentous, suppression by *Saccharomyces cerevisiae* transposons, 671

Herbicide resistance, in *Arabidopsis thaliana*, fitness consequences, 807
Heteroduplex formation, *Minos* transposon mobilization in *Drosophila melanogaster*, 267
Heterozygotes, selection against, spread of advantageous alleles across barriers, 493
Humans
constant T-cell receptor evolution, 409
estimation of number of immunoglobulin V-genes in, 777
geographic distribution of Y chromosome variation, 787
Hybrids/hybridization
Drosophila hybrid inviability, 1031
sterility and breakdown in *Oryza sativa*, 1139
Hydractinia symbiolongicarpus, control of allogenicity specificity (*letter*), 857

Immunoglobulin V-genes, method of estimating numbers in mice and humans, 777
Introgression analysis, quantitative trait loci contributing to morphological difference between *Drosophila simulans* and and *Drosophila mauritiana*, 339
Introns, circular, cytosolic ribosomal mutations abolishing accumulation in *Podospora anserina* without preventing Senescence, 697
Isolation, genetic differentiation and estimation of gene flow from *F*-statistics under, 1219
Isolation model, estimation of ancestral population parameters, 847

Kinship Program, 535

Letter to the Editor, control of allogenicity specificity in *Hydractinia symbiolongicarpus*, 857
Long terminal repeats, increased length of, Ty1 transposition inhibition and tandem multimer formation and, 911

Maize
Ac/D transposon formation, structure, and fate, 1161
location of genes governing long first internode, 1149
tha1 gene, *in vivo* role of cp-SecA in thylakoid protein targeting, 467
Major histocompatibility complex, genetic variation in bighorn sheep, 421
Mammals, olfactory receptor gene evolution, 185
Mapping
of Muller's elements D and E in *Drosophila repleta,* 281
of quantitative trait loci using historical recombinations, 1201
Meiosis
asymmetrical isochromosome development and meiotic behavior in wheat, 1155
in *Caenorhabditis elegans* germ line, *glp-3* requirement for, 111
Saccharomyces cerevisiae
competition between adjacent recombination hotspots, 661
histone H2A-H2B dimer concentration and progression into, 647
Meyerowitz, Elliot, Genetics Society of America Medal awarded, 1
Mice. *See also Mus musculus*
Bmp5 mutations, 435
constant T-cell receptor evolution, 409
estimation of number of immunoglobulin V-genes in, 777
masculinizer mutation definition of sex-determining gene, 173
mitochondrial genotype segregation in heteroplasmic lineage, embryonic karyoplast transplantation producing, 445
Microsatellite loci
genetic variation in bighorn sheep, 421
range constraints, 207
Minos transposon, mobilization in *Drosophila melanogaster,* 267
Mismatches, *Escherichia coli* transformation, 29
Mitochondria
Culaea inconstans, DNA duplications, 383
DNA segregation in mice, embryonic karyoplast transplantation producing, 445
male-dependent doubly uniparental inheritance of DNA in *Mytilus galloprovincialis,* 1073
origins of mutation conferring deafness, 771
Saccharomyces cerevisiae cytochrome *c* oxidase subunit II of, deletion of leader peptide of precursor of, 903
Mitosis
in *Caenorhabditis elegans* germ line, *glp-3* requirement for, 111
Drosophila hybrid inviability, 1031
Saccharomyces cerevisiae PPH2 mutants, 227
Ustilago maydis REC2 and *RAD51* genes, 243
Mitotis, *Saccharomyces cerevisiae* Swi5 regulation of exit from, 85
Models. *See also* Animal models; *specific models*
estimation of ancestral population parameters, 847
genealogies under selection, 519
of mutation and selection, coexistence of multiple alleles and, 1171
random genetic drift, 485
Muller's elements D and E, mapping in *Drosophila repleta,* 281
Musca domestica, masculinizer mutation definition of sex-determining gene, 173
Mus musculus, lethal *t*-haplotype polymorphism in, impact of migration and fitness on stability, 1093
Mutants/mutation
adaptive, specificity, 39
Bmp5, in mice, 435
cytosolic ribosomal mutations abolishing accumulation of circular intron in *Podospora anserina* without preventing Senescence, 697
det1, identification of elements of flowering-time and light-response regulatory pathways by extragenic suppressors in *Arabidopsis thaliana,* 1125
dnaG, in *Escherichia coli,* isolation and characterization of suppressors, 867
estimation of number of immunoglobulin V-genes, 777
Fisherian mutation, 1171
masculinizer, sex-determining gene determination in *Musca domestica,* 173
mod(mdg4), in *Drosophila,* characterization of functional domains of su(Hw) protein mediating silencing effect of, 153
nudC3, $tRNA^{Leu}$ missense suppressor, 707
1555G, mitochondrial, conferring deafness, 771
parB, in *Escherichia coli,* isolation and characterization of suppressors, 867
petD, suppression by *SIM30* in *Chlamydomonas reinhardtii,* 935
PP1 alanine-scanning mutagenesis, 615
Saccharomyces cerevisiae PPH2, 227
Saccharomyces cerevisiae transposons, filamentous growth suppression by, 671
Salmonella P22, abortive transduction, 17
SIM30, translational defect suppression in *Chlamydomonas reinhardtii* by, 935
TnsC, gain-of-function, 573
trp1, of *Arabidopsis thaliana,* 197
ultraviolet-induced, 863
Mytilus galloprovincialis
female-dependent sex-ratio in, 1073
male-dependent doubly uniparental inheritance of mitochondrial DNA in, 1073

Nuclear migration, in *Aspergillus nidulans,* $tRNA^{Leu}$ missense suppressor of nudC3 blocking, 707

Nucleotide variation, at glucose dehydrogenase locus in *Drosophila melanogaster,* 1053

Olfactory receptor genes, mammalian evolution, 185
Oogenesis, *Drosophila* ovarian ring canal inner rim formation dependence on *cheerio,* 1063
Origin recognition complex (ORC), Sas2 role in functioning, 923
Oryza sativa
  grain yield components, epistasis with quantitative trait loci, 453
  hybrid sterility and breakdown, 1139
Ovarian ring canal, *Drosophila,* inner rim formation dependence on *cheerio,* 1063
Ovule development, in *Arabidopsis thaliana,* interaction among genes regulating, 1109

Paramecium genetics (*Perspectives*), 217
Perspectives
  Paramecium genetics, 217
  P element invasions, 11
  retrotransfer and conjugation, 543
  ultraviolet-induced mutation and chemical nature of genes, 863
Phenotypic traits, multilocus and multitrait measures of differentiation for, 1229
Pheromones
  Caenorhabditis elegans dauer-inducing pheromone, G protein chemosensation of, 715
  sexual isolation between *Drosophila mauritiana* and *Drosophila sechellia* and, 1015
Phylogeny, ribosomal DNA evolution, 821
Pigs, single genes affecting meat quality traits, Bayesian statistical analysis for, 395
Plants, logic of development, 5
Podospora anserina, cytosolic ribosomal mutations abolishing accumulation of circular intron in, without preventing Senescence, 697
Polymorphism
  decapentaplegic gene sequence polymorphism and species divergence in *Drosophila melanogaster,* 311
  lethal *t*-haplotype polymorphism in *Mus musculus,* impact of migration and fitness on stability, 1093
  sequence in *Escherichia coli,* bacterial interspersed mosaic elements as source, 551
Population genetics
  coalescent estimator of population recombination rate, 833
  decapentaplegic gene sequence polymorphism and species divergence in *Drosophila melanogaster,* 311
  estimation of ancestral population parameters, 847
  genealogy of samples in models with selection, 519
  genetic differentiation and estimation of gene flow from *F*-statistics under isolation, 1219 by distance
  geographic distribution of Y chromosome variation in humans, 787
  nucleotide variation at glucose dehydrogenase locus in *Drosophila melanogaster,* 1053
  random genetic drift
    models, 485
    spread of advantageous alleles across barriers, 493
Population recombination rate, coalescent estimator, 833
Position effect variegation (PEV), heterochromatic factors in *Drosophila melanogaster,* 945
Position effect variegation, *trans*-suppression in *Drosophila* minimicrosomes, 325
Posterior lobe, quantitative trait loci contributing to morphological difference between *Drosophila simulans* and and *Drosophila mauritiana,* 339
Pyruvate decarboxylase, *pdc2* regulation, suppression in *Saccharomyces cerevisiae,* 587

Quantitative trait loci (QTL)
  contributing to morphological difference between *Drosophila simulans* and and *Drosophila mauritiana,* introgression analysis of, 339
  mapping using historical recombinations, 1201
  rice grain yield component epistasis, 453

Rainbow trout, secondary tetrasomic segregation of *MDH-B* and preferential pairing of homeologues in, 1083
Random genetic drift
  models, 485
  spread of advantageous alleles across barriers, 493
Range constraints, microsatellite loci, 207
Recombination
  historical, mapping of quantitative trait loci using, 1201
  meiotic, *Saccharomyces cerevisiae,* competition between adjacent hotspots, 661
  mismatch repair transformation by highly mismatched molecules resembling recombination intermediates in *Escherichia coli,* 29
  multilocus evolution in fire ants, 961
  "parahomologous" gene targeting in *Drosophila,* 349
Replication Protein-A, subunit role in DNA replication force movement in *Saccharomyces cerevisiae,* 891
Restriction fragment length polymorphism, epistasis with quantitative trait loci in rice, 453
Retrotransfer (*Perspectives*), 543
Ribosomes
  cytosolic mutations abolishing accumulation of circular intron in *Podospora anserina* without preventing Senescence, 697
  evolution of DNA, divergent paralogues and phylogenetic implications, 821
Rice. *See also Oryza sativa*
  grain yield components, epistasis with quantitative trait loci, 453

Saccharomyces cerevisiae
chromosome loss caused by *SIR* gene hyperactivation, 605
cytochrome *c* oxidase subunit II of, deletion of leader peptide of precursor of, 903
DNA replication fork movement, replication Protein-A subunits in, 891
filamentous growth suppression by transposon mutagenesis, 671
high affinity sulfate transporters, molecular characterization, 627
MDP1 identity with *RSP4*, 595
meiosis
competition between adjacent recombination hotspots, 661
histone H2A-H2B dimer concentration and progression into, 647
PKC1 encoding of glycosyltransferase, 637
PPH2 mutants, 227
PP1 mutagenesis, 615
Rim1p regulation of sporulation in, 63
Sas2 role in silencing and origin recognition complex functioning, 923
S phase regulation in response to DNA damage, *RAD9*, *RAD17*, and *RAD24* requirement for, 45
suppression of *pdc2* regulation of pyruvate decarboxylase synthesis, 587
Swi5 regulation of Sic1 and mitotic exit, 85
transcriptional silencing and switching competence in, epigenetic inheritance of, 685
Salmonella spp., P22 abortive transduction mutant, 17
Salmonella typhimurium, deletion formation between flagellin genes, 551
Schizophyllum commune, specificity region of Y proteins, 253
Schizosaccharomyces pombe, glutathione-mediated detoxification in, 75
Segregation analysis, genotype probability index derived from, 479
Selection, multilocus evolution in fire ants, 961
Senescence, cytosolic ribosomal mutations abolishing accumulation of circular intron in *Podospora anserina* without preventing, 697
Sequence polymorphism
decapentaplegic gene in *Drosophila melanogaster*, 311
Escherichia coli, bacterial interspersed mosaic elements as source, 551
Sex ratio, female-dependent, in *Mytilus galloprovincialis*, 1073
Sheep, major histocompatibility complex and microsatellite loci variation, 421
Signal transduction
hedgehog, *oroshigane* functions, 1041
torso, in *Drosophila*, D-raf effects, 163
Silencing
Drosophila mod(mdg4) mutations effects, characterization of functional domains of su(Hw) protein mediating, 153
Saccharomyces cerevisiae, epigenetic inheritance of, 685
Sas2 role, 923
Size-change model, estimation of ancestral population parameters, 847
Solenopsis invicta, multilocus evolution in, 961
Spectinomycin, *Chlamydomonas reinhardtii* resistance to, eubacterial gene conferring, 95
Sperm, precedence in *Drosophila melanogaster*, quantitative genetics, 139
Sporulation, Rim1p regulation in yeasts, 63
Stahl, Franklin W., Thomas Hunt Morgan Medal awarded, 1
Sulfate transporters, high affinity, in *Saccharomyces cerevisiae*, molecular characterization, 627

T-cell receptors, evolution of gamma and delta constant regions, in human-rodent-artiodactyl triplet, 409
Tetrasomy, secondary tetrasomic segregation of *MDH-B* and preferential pairing of homeologues in rainbow trout, 1083
Thomas Hunt Morgan Medal, awarded to Franklin W. Stahl, 1
Thylakoid membrane, maize, *tha1* transposon insertion, 467
TRAM retransposon, location in *Drosophila miranda*, 261
Transcription, silencing and switching competence in fission yeast, epigenetic inheritance of, 685
Transcription factors, *Saccharomyces cerevisiae* Swi5 regulation of Sic1 and mitotic exit, 85
Transduction, abortive, *Salmonella* P22 mutant defective in, 17
Translation, *Chlamydomonas reinhardtii* defects in, *SIM30* mutation suppression of, 935
Transposable elements, *P* element invasions in *Drosophila melanogaster* (*Perspectives*), 1111
Transposition, Ty1 transposition inhibition by increased length of long terminal repeats, 911
Transposons
Ac/D, formation, structure, and fate, 1161
Minos, mobilization in *Drosophila melanogaster*, 267
mutagenesis in *Saccharomyces cerevisiae*, filamentous growth suppression by, 671
tha1, insertion, 467
Tn7, TnsC activation, 573
TRAM retransposon, location in *Drosophila miranda*, 261
Ty1 retrotransposon, inhibition by increased length of long terminal repeats, 911
Triticum aestivum, asymmetrical isochromosome development and meiotic behavior, 1155

Ultraviolet light, mutation induced by (*Perspectives*), 863
Uniparental inheritance, male-dependent, of mitochondrial DNA in *Mytilus galloprovincialis*, 1073

Ustilago maydis, REC2 and *RAD51* genes in DNA repair and mitotic recombination, 243

Variance components, estimation from data containing inbred individuals in common carp, 1243

Wheat, asymmetrical isochromosome development and meiotic behavior, 1155

Y chromosomes
human, geographic distribution of variation, 787
neo-Y-chromosome of *Drosophila americana americana,* lack of degeneration of loci on, 989
TRAM retransposon location in *Drosophila miranda,* 261

Yeasts. *See also Saccharomyces cerevisiae*
glutathione-mediated detoxification in, 75
Rim1p regulation of sporulation in, 63

Y proteins, *Schizophyllum commune,* specificity region, 253

Zea mays, location of genes governing long first internode, 1149